



SEQUENCE LISTING

<110> REED, ROBIN
ZHOU, ZHAOLAN

<120> PURIFICATION OF FUNCTIONAL RIBONUCLEOPROTEIN COMPLEXES

<130> HMV-080.01

<140> 10/047,991

<141> 2002-01-14

<150> 60/261,521

<151> 2001-01-12

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 393

<212> DNA

<213> Enterobacteria phage MS2

<220>

<221> CDS

<222> (1) .. (390)

<400> 1

atg gct tct aac ttt act cag ttc gtt ctc gtc gac aat ggc gga act	48
Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr	
1 5 10 15	
ggc gac gtg act gtc gcc cca agc aac ttc gct aac ggg gtc gct gaa	96
Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu	
20 25 30	
tgg atc agc tct aac tcg cgt tca cag gct tac aaa gta acc tgt agc	144
Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser	
35 40 45	
gtt cgt cag agc tct gcg cag aat cgc aaa tac acc atc aaa gtc gag	192
Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu	
50 55 60	
gtg cct aaa gtg gca acc cag act gtt ggt ggt gta gag ctt cct gta	240
Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val	
65 70 75 80	
gcc gca tgg cgt tcg tac tta aat atg gaa cta acc att cca att ttc	288
Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe	
85 90 95	
gct acg aat tcc gac tgc gag ctt att gtt aag gca atg caa ggt ctc	336
Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu	
100 105 110	

cta aaa gat gga aac ccg att ccc tca gca atc gca gca aac tcc ggc 384
 Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

atc tac taa 393
 Ile Tyr
 130

<210> 2
 <211> 130
 <212> PRT
 <213> Enterobacteria phage MS2

<400> 2
 Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
 1 5 10 15
 Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 20 25 30
 Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
 35 40 45
 Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
 50 55 60
 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 65 70 75 80
 Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 85 90 95
 Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110
 Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125
 Ile Tyr
 130

<210> 3
 <211> 1380
 <212> DNA
 <213> Escherichia coli

<400> 3
 tacgttttcg cgtttttaggc cggacaaggc gttcacgccg catccggcat ttcacagcat 60
 tacttggtga tacgagtctg cgcgtctttc agggcttcat cgacagtctg acgaccgctg 120
 gcggcggtga tcaccgcagt acgcacggca taccagaaag cggacatctg cgggatgttc 180
 ggcatgattt cacctttctg ggcgttttcc atggtggcgg caatacgtgg atctttcgcc 240
 aactcttcct cgtaagactt cagcgctacg gcaccacg cgtttgtctt attaaccgct 300
 tccagacctt catcagtcag cagatagttt tcgaggaact ctttcgccag ctctttgttc 360
 ggactggcgg cgттааtacc tgcgctcagc acgccaacga acggtttgga tgggtgacct 420
 ttgaaggctg gcagtaccgt tacaccataa ttacttttgc tgggtgctgat gttggacct 480
 gccacgggc cgttgatggg catcgctggt tcgcctttat taaaggcagc ttctgcgatg 540

gagtaatcgg tgtctgcatt catgtgtttg tttttaatca ggtcaaccag gaaggtcaga 600
 cccgcttttcg cgccagcggt atccacgccc acgtctttaa tgcgtactt gccgttttca 660
 tacttgaacg cataaccccc gtcagcagca atcagcggcc aggtgaagta cggttcttgc 720
 aggttgaaca tcagcgcgct cttacctttc gctttcagtt ctttatccag cgccgggac 780
 tcttcccagg tttttggcgg gtccggcagc agatctttgt tataaatcag cgataacgct 840
 tcaacagcga tcgggtaagc aatcagcttg ccgttgtaac gtacggcatc ccaggtaaac 900
 ggatacagct tgtcctggaa cgctttgtcc ggggtgattt cagccaacag gccagattga 960
 gcgtagccac caaagcggtc gtgtgcccag aagataatgt cagggccatc gccagttgcc 1020
 gcaacctgtg ggaatttctc ttccagttta tccggatgct caacgggtgac tttaattccg 1080
 gtatctttct cgaatttctt accgacttca gcgagaccgt tatagccttt atcgccgtta 1140
 atccagatta ccagtttacc ttcttcgatt ttggcgagag ccgaggcgga aaacatcatc 1200
 gtcgttaatg cggataatgc gaggatgcgt gcacctgttt ttattttcat aatctatggg 1260
 ccttggttgg gaagtgtctg tgaacacacc taaacggact ctagtttctt tatacgcaa 1320
 cctctttcca tctccttgc ccctacgccc caccgtcgct ttgtgtgatc tctgttacag 1380

<210> 4

<211> 396

<212> PRT

<213> Escherichia coli

<400> 4

Met	Lys	Ile	Lys	Thr	Gly	Ala	Arg	Ile	Leu	Ala	Leu	Ser	Ala	Leu	Thr
1				5					10					15	
Thr	Met	Met	Phe	Ser	Ala	Ser	Ala	Leu	Ala	Lys	Ile	Glu	Glu	Gly	Lys
			20					25					30		
Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys	Gly	Tyr	Asn	Gly	Leu	Ala	Glu
	35					40						45			
Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	Gly	Ile	Lys	Val	Thr	Val	Glu
	50					55					60				
His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly
65					70				75					80	
Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	His	Asp	Arg	Phe	Gly	Gly	Tyr
			85						90					95	
Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	Thr	Pro	Asp	Lys	Ala	Phe	Gln
			100					105					110		
Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys
	115						120					125			
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn
	130					135					140				
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala
145					150					155				160	
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn
			165					170						175	
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly
		180						185					190		

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys
 340 345 350
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
 355 360 365
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
 370 375 380
 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
 385 390 395

<210> 5
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
 caggatcatat gggatccgcgg gcttctaact ttactcagtt cggt

<210> 6
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
 tgctactcga gggcgctagc gtagatgccg gagtttgctg cgat

44

<210> 7
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 recognition oligonucleotide

<400> 7
 cgtacaccat cagggtacg

19

<210> 8
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 fusion peptide

<400> 8
 Leu Val Pro Arg Gly Ser His Met Arg Gly Ser His His His His His
 1 5 10 15
 His

<210> 9
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 thrombin cleavage site peptide

<400> 9
 Leu Val Pro Arg Gly Ser His
 1 5

<210> 10
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 10
 Met Arg Gly Ser His His His His His
 1 5 10

<210> 11
 <211> 455
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide sequence

<400> 11
 taatacgact cactataggg agaccggcag atcagcttgg ccgcgtccat ctggatcatct 60
 aggatctgat atcatcgatg aattcgagct cggtagcccg ttcgtcctca ctctcttccg 120
 catcgctgtc tgcgagggcc agctgttggg gtgagtactc cctctcaaaa gcgggcatga 180
 cttctgccct cgagttatta accctcacta aaggcagtag tcaagggttt ccttgaagct 240
 ttcgtgctga cctgtccct ttttttcca cagctgcagg tcgacgttga ggacaaactc 300
 ttcgcggtct ttccagtact cttggatccg atatccgtac accatcaggg tacgagctag 360
 cccatggcgt acaccatcag ggtacgacta gtagatctcg tacaccatca gggtagggaa 420
 ttctctagag tcgagttcta tagtgcacc taaat 455

<210> 12
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 6x His tag

<400> 12
 His His His His His His
 1 5